

5. The method according to claim 4, wherein said coding region comprises a nucleotide sequence selected from the group consisting of
- 5 a nucleotide sequence comprising at least 19 or 25 contiguous nucleotides having at least 70 % sequence identity to a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2 or the complement thereof; and
- 10 a nucleotide sequence comprising at least 25 contiguous nucleotides having at least 70 % sequence identity to a nucleotide sequence encoding a polypeptide comprising the nucleotide sequence of SEQ ID No 1 or the complement thereof.
6. The method according to claim 5, wherein said coding region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide at position 2208
- 15 to the nucleotide at position 2598 or the complement thereof.
7. The method according to claim 5, wherein said coding region comprises both sense and antisense nucleotide sequences capable of forming a double stranded RNA molecule.
- 20 8. The method according to any one of claims 1 to 7, wherein said promoter is a subterranean clover stunt virus promoter.
9. The method according to any one of claims 1 to 7, wherein said fiber-
- 25 producing plant is a cotton plant.
10. The method according to claim 8, wherein said fiber-producing plant is a cotton plant.
- 30 11. The method according to claim 9, wherein said cotton plant is a FibermaxTM variety.

12. A method for improving fiber yield in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

- 5 a plant expressible promoter;
 a DNA region capable of being translated into an active sucrose
 synthase protein; and
 a transcription termination and polyadenylation signal which functions in
 said plant cells.

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13. A method for improving fiber quality in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments

- a plant expressible promoter;
15 a DNA region capable of being translated into an active sucrose
 synthase protein; and
 a transcription termination and polyadenylation signal which functions in
 said plant cells.

20 14. A method for increasing seed size in a fiber-producing plant, comprising providing cells of said plant with a chimeric gene comprising the following operably linked DNA fragments:

- a seed-specific promoter;
 a DNA region capable of being translated into an active sucrose
25 synthase protein; and
 a transcription termination and polyadenylation signal which functions in
 said plant cells.

15. A fiber-producing plant comprising in its genome a chimeric DNA
30 comprising the following operably linked DNA fragments:
 a plant expressible promoter;

a coding region which when transcribed yields an RNA said RNA being capable of reducing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells; or
 5 capable of being translated into an active sucrose synthase protein; and
 a transcription termination and polyadenylation signal which functions in said plant cells.

10 16. A fiber-producing plant according to claim 15, wherein said RNA is capable of increasing the expression of an endogenous sucrose synthase gene, preferably an endogenous sucrose synthase gene expressed in fiber cells, preferably fiber initial cells and said fiber cells have an increased sucrose synthase activity compared to fiber cells of plant cells which do not comprise
 15 said chimeric DNA.

17. The fiber-producing plant according to claim 16, wherein said coding region comprises a nucleotide sequence selected from
 20 a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID No 2;
 b) a nucleotide sequence comprising the nucleotide sequence of SEQ ID No 1;
 c) a nucleotide sequence having at least 70% sequence identity with the nucleotide sequence a) or b);
 25 d) a nucleotide sequence hybridizing under stringent conditions with the nucleotide sequence a) or b);
 or a part thereof encoding an active sucrose synthase.

18. A fiber-producing plant according to claim 15, wherein said RNA is
 30 capable of reducing an endogenous sucrose synthase gene and said fiber cells

have a reduced sucrose synthase activity compared to fiber cells of plant cells which do not comprise said chimeric DNA.

19. The fiber-producing plant according to claim 18, wherein said coding
 5 region comprises a nucleotide sequence selected from the group consisting of
 a nucleotide sequence comprising at least 19 or 25 contiguous
 nucleotides having at least 70 % sequence identity to a nucleotide
 sequence encoding a polypeptide comprising the amino acid sequence
 of SEQ ID No 2 or the complement thereof; and
 10 a nucleotide sequence comprising at least 19 or 25 contiguous
 nucleotides having at least 70 % sequence identity to a nucleotide
 sequence encoding a polypeptide comprising the nucleotide sequence of
 SEQ ID No 1 or the complement thereof.
- 15 20. The fiber-producing plant according to claim 18, wherein said coding
 region comprises the nucleotide sequence of SEQ ID No 1 from the nucleotide
 at position 2208 to the nucleotide at position 2598 or the complement thereof.
21. The fiber-producing plant according to any one of claims 15 to 20,
 20 wherein said plant is a cotton plant.
22. Seeds of a plant according to any one of claims 15 to 20.
23. Seeds of a plant according to claim 21.
- 25 24. Fibers with altered development or properties, isolated from plants
 according to any one of claims 15 to 20.
25. Fibers with altered development or properties, isolated from plants
 30 according to claim 21.

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